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W P S R L H (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Thu Aug 6 14:08:28 1998; MasPar time 13.37 Seconds  
Tabular output not generated. 765.547 Million cell updates/sec

Title: >US-08-813-323A-1  
Description: (324-566) from US08813323A.pep (3 of 3)  
Perfect Score: 1764  
Sequence: 1 SOAEKLKELDKREIRPFQNW.....YIKDDTIFIKVIVTSDLPD 243

Scoring table: PAM 150  
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrembl6  
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal  
5:sp\_mhc 6:sp\_organelle 7:sp\_phase 8:sp\_plant  
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertibrate  
13:sp\_unclassified

Statistics: Mean 45.863; Variance 93.351; scale 0.491

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1764	100.0	567	10	Q60803	TNF RECEPTOR-ASSOCIATE
2	1758	99.7	567	10	Q62380	TNF RECEPTOR-ASSOCIATE
3	1754	99.4	568	2	Q13076	LMP1 ASSOCIATED PROTEIN
4	1754	99.4	568	2	Q13114	CD40 RECEPTOR ASSOCIAT
5	1747	99.0	543	2	Q13947	CD40-ASSOCIATED PROTEIN
6	1740	98.5	567	2	Q12990	CD40 BINDING PROTEIN
7	909	51.5	558	10	P70191	TNF RECEPTOR-ASSOCIATE
8	908	51.5	558	10	Q61480	TNF RECEPTOR-ASSOCIATE
9	894	50.7	538	2	Q00453	TNF RECEPTOR ASSOCIATE
10	730	41.4	416	2	Q13077	EPSTEIN-BARR VIRUS-IND
11	663	37.6	501	2	Q12933	TUMOR NECROSIS FACTOR
12	437	24.8	470	2	Q14848	CYSTINE RICH DOMAIN AS
13	407	23.1	470	10	Q61382	CYSTINE RICH MOTIF AS
14	337	19.1	530	10	P70196	TNF RECEPTOR-ASSOCIATE
15	117	6.6	284	3	Q16188	TROPOMYOSIN
16	117	6.6	289	3	Q18416	TROPOMYOSIN
17	117	6.6	299	3	Q23939	MAG44 (FRAGMENT)
18	114	6.5	284	12	Q91472	FAST MUSCLE TROPOMYOSI
19	113	6.4	248	10	Q63608	ALPHA-TROPOMYOSIN 5A
20	113	6.4	248	10	Q63609	ALPHA-TROPOMYOSIN 5B

21	113	6.4	535	9	P72839	HYPOTHETICAL 61.7 KD P	2.42e-02
22	113	6.4	4096	2	Q13327	DNA DEPENDENT PROTEIN	2.42e-02
23	113	6.4	4127	2	P78527	DNA-DEPENDENT PROTEIN	2.42e-02
24	111	6.3	847	2	Q16584	PROTEIN KINASE	4.45e-02
25	111	6.3	1060	10	Q62036	5-AZACYTIDINE INDUCED	4.45e-02
26	110	6.2	284	3	Q25145	TROPOMYOSIN	6.02e-02
27	110	6.2	538	3	Q25616	CIRCULATING ANTIGEN	6.02e-02
28	109	6.2	772	3	Q23529	SIMILAR TO PARAMYOSIN	8.13e-02
29	107	6.1	204	10	P70525	RAT STRIATED MUSCLE AL	1.47e-01
30	107	6.1	243	2	Q15657	TROPOMYOSIN ISOFORM	1.47e-01
31	107	6.1	280	10	P70524	RAT SMOOTH MUSCLE ALPH	1.47e-01
32	107	6.1	284	12	Q91490	SLOW MUSCLE TROPOMYOSI	1.47e-01
33	107	6.1	284	12	Q90348	CARDIAC TROPOMYOSIN	1.47e-01
34	107	6.1	284	10	Q63582	NON-MUSCLE ALPHA TROPO	1.47e-01
35	107	6.1	284	10	Q63607	ALPHA-TROPOMYOSIN 3	1.47e-01
36	107	6.1	284	10	Q63583	HEPATOMA ALPHA TROPOMY	1.47e-01
37	107	6.1	338	2	Q00377	L1 ELEMENT L1.39 P40 A	1.47e-01
38	107	6.1	338	2	Q00374	L1 ELEMENT L1.25 P40 A	1.47e-01
39	107	6.1	981	8	O04612	A-IG002N01.24	1.47e-01
40	108	6.1	1410	3	Q20439	T18D3.4 (FRAGMENT)	1.10e-01
41	106	6.0	337	2	Q00373	L1 ELEMENT L1.24 P40	1.98e-01
42	106	6.0	510	3	Q24425	TROPOMYOSIN GENE ISOFO	1.98e-01
43	106	6.0	633	3	Q17048	CYTOPLASMIC INTERMEDIA	1.98e-01
44	106	6.0	2648	3	Q18291	ZK1151.2	1.98e-01
45	106	6.0	3187	10	Q63714	RAT GCP360	1.98e-01

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	567	AA
AC	Q60803				
DT	01-NOV-1996	(TREMBLREL. 01, CREATED)			
DT	01-NOV-1996	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998	(TREMBLREL. 01, LAST ANNOTATION UPDATE)			
DE	TNF RECEPTOR-ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1).				
GN	TRAF3 OR CRAFT				
OS	MUS MUSCULUS (MOUSE)				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	CHENG G., CLEARY A.M., YE Z., HONG D.I., LEDERMAN S., BALTIMORE D.;				
RL	SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.				
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.				
DR	EMBL; U21050; G719293; -				
DR	MGI; MGI:108041; TRAF3.				
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.				
KW	ZINC-FINGER.				
SQ	SEQUENCE 567 AA; 64263 MW; F85A30F3 CRC32;				

Query Match	100.0%	Score	1764	DB	10	Length	567
Best Local Similarity	100.0%	Pred. No.	0.00e+00				
Matches	243	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Db	324	SOAEKLKELDKREIRPFQNW	EEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ	383			
Qy	324	SOAEKLKELDKREIRPFQNW	EEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ	383			
Db	384	LSRHDQTLVSHDIRLADMDLRFVLETASYNGVLWIKIRYKRRKQBAVMGKTLISLSQ	443				
Qy	384	LSRHDQTLVSHDIRLADMDLRFVLETASYNGVLWIKIRYKRRKQBAVMGKTLISLSQ	443				
Db	444	FYTGIFYGKMCARYLNGDGMKGKTHLSLFFVIMRGYDALLPFPFKQKVTMLMDQSS	503				
Qy	444	FYTGIFYGKMCARYLNGDGMKGKTHLSLFFVIMRGYDALLPFPFKQKVTMLMDQSS	503				
Db	504	RRHLGDAFKPDPNSSSFKPTGEMNIASGCPVFAQVLENGTYIKDDTIFIKVIVTSD	563				
Qy	504	RRHLGDAFKPDPNSSSFKPTGEMNIASGCPVFAQVLENGTYIKDDTIFIKVIVTSD	563				
Db	564	LPD 566					

QY 564 LPD 566

## RESULT 2

ID Q62380 PRELIMINARY; PRT; 567 AA.  
 AC Q62380;  
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)  
 DE TNF RECEPTOR-ASSOCIATED FACTOR 3 (TRAFAMN).  
 GN TRAF3 OR TRAFAMN.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE-BRAIN;  
 RA WANG X., BORNISLAAGER E., HAUB O., TOMIHARA-NEUBERGER C.,  
 RA LONBERG N., DINULOS M.B., DISTECHE C.M., COPELAND N.,  
 RA GILBERT D.J., JENKINS N.A., LACY E.;  
 RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; U33840; G1488198;  
 DR MGD; MGI:108041; TRAF3.  
 SQ SEQUENCE 567 AA; 64376 MW; 7F4F873B CRC32;

Query Match 99.7%; Score 1758; DB 10; Length 567;

Best Local Similarity 99.6%; Pred. No. 0.00e+00; Mismatches 0; Indels 0; Gaps 0;

Matches 242; Conservative 0; Indels 0; Gaps 0;

Db 324 SOAEKLEKELDKIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 383

QY 324 SOAEKLEKELDKIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 383

Db 384 LSRHDOMLSVHDIRLADMDLRFOVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 443

QY 384 LSRHDOMLSVHDIRLADMDLRFOVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 443

Db 444 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMMDQSS 503

QY 444 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMMDQSS 503

Db 504 RRLHDAFKPDNPSSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDDTIFIKVIVDTSD 563

QY 504 RRLHDAFKPDNPSSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDDTIFIKVIVDTSD 563

Db 564 LPD 566

QY 564 LPD 566

## RESULT 3

ID Q13076 PRELIMINARY; PRT; 568 AA.  
 AC Q13076;  
 DT 01-NOV-1996 (TREMELREL. 01, CREATED)  
 DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)  
 DE LMP1 ASSOCIATED PROTEIN.  
 OS HOMO SAPIENS (HUMAN).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LYMPHOID TUMOR;  
 RX MEDLINE; 95163092.  
 RA MOSTALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C.,  
 RA KIEFF E.;  
 RL CELL 80:389-399(1995).  
 CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.  
 DR EMBL; U19260; G675460;  
 DR PROSITE; P800518; ZINC\_FINGER\_C3HC4; 1.  
 KW ZINC-FINGER.  
 SQ SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;

Query Match 99.4%; Score 1754; DB 2; Length 568;

Best Local Similarity 99.2%; Pred. No. 0.00e+00;

Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SOAEKLEKELDKIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 384

QY 324 SOAEKLEKELDKIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 383

Db 385 LSRHDOMLSVHDIRLADMDLRFOVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 444

QY 384 LSRHDOMLSVHDIRLADMDLRFOVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 443

Db 445 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMMDQSS 504

QY 444 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMMDQSS 503

Db 505 RRLHDAFKPDNPSSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDDTIFIKVIVDTSD 564

QY 504 RRLHDAFKPDNPSSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDDTIFIKVIVDTSD 563

Db 565 LPD 567

QY 564 LPD 566

## RESULT 4

ID Q13114 PRELIMINARY; PRT; 568 AA.

AC Q13114;

DT 01-NOV-1996 (TREMELREL. 01, CREATED)

DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)

DE CD40 RECEPTOR ASSOCIATED FACTOR 1.

GN CRAFT.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95184010.

RA CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D.;

RL SCIENCE 267:1494-1498(1995).

CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL; U21092; G726088;

DR PROSITE; P800518; ZINC\_FINGER\_C3HC4; 1.

KW ZINC-FINGER.

SQ SEQUENCE 568 AA; 64460 MW; 77A8CBDB CRC32;

Query Match 99.4%; Score 1754; DB 2; Length 568;

Best Local Similarity 99.2%; Pred. No. 0.00e+00;

Matches 241; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 325 SOAEKLEKELDKIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 384

QY 324 SOAEKLEKELDKIRPFRQNWEEADSMKSSVESLQNRVTELESVDKSAQAARNTGLLESQ 383

Db 385 LSRHDOMLSVHDIRLADMDLRFOVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 444

QY 384 LSRHDOMLSVHDIRLADMDLRFOVLETASVNGVLWKIRDYKRRKQEA VMGKTLISLQSP 443

Db 445 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMMDQSS 504

QY 444 FYTGFGYKMCARVYLGDMGKGTHLSLFFVIMRGEYDALLPWPFKOKVTLMMDQSS 503

Db 505 RRLHDAFKPDNPSSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDDTIFIKVIVDTSD 564

QY 504 RRLHDAFKPDNPSSSFKKPTGEMNIASGCPVFVAQTVLNGTYIKDDTIFIKVIVDTSD 563

Db 565 LPD 567

QY 564 LPD 566

## RESULT 5



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DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE TNF RECEPTOR-ASSOCIATED FACTOR 5 (TRAF5).
GN TRAF5.
OS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE; 96278943.
RA NAKANO H., OSHIMA H., CHUNG W., WILLIAMS-ABBOTT L., WARE C.F.,
RA YAGITA H., OKUMURA K.,
RL J. BIOL. CHEM. 271:14661-14664(1996).
CC -I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; D78141; G1469893; -.
DR MGI; 107548; TRAF5.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
KW ZINC-FINGER.
SQ SEQUENCE 558 AA; 64154 MW; 910ACC60 CRC32;

Query Match 51.5%; Score 908; DB 10; Length 558;
Best Local Similarity 50.4%; Pred. No. 1.15e-152;
Matches 124; Conservative 58; Mismatches 59; Indels 5; Gaps 4;

Db 314 SHYDRSNALEAQRHLLQI-VNQPSRLDLSLVDVSVKQRIQTLEASDQRLV-LLEG 371
QY 324 SQAELKELDKETPRFRQNEEADSMKSVESLQNRVTEL-ESVDKSAGQAARNTGLLES 382
Db 372 ETSKDHAINIKHAOLNKEERFKLEGACYSGLIKLVTDYRVKKREAVEGHTVSFVSQ 431
QY 383 QLSRHDTLSVHDRLADMDLRFQVLETASVNGVLWKIRDYKRRKQAVMGKTLISLSQ 442
Db 432 PFYTSRCYRLCARAYLNGDGSKGTHLSLYFVVMRGEFDSLLQWPFQRVRLMLDQSG 491
QY 443 PFYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRGEYDALLPWFQKQVTLMLDQGS 502
Db 492 KKHIVETKADPNSSFRPQGMNIASGCPFRVSHSTLENSKTYIKDDTLFLKVAVD 551
QY 503 SRRLGDFAKPDPPNSSFSFKPTGEMNIASGCPVFAQTVLENG--TYIKDDTIFIKVID 560
Db 552 LTDLSD 557
QY 561 TSDLPD 566

RESULT 9
ID 000463 PRELIMINARY; PRT; 538 AA.
AC 000463.
DT 01-JUL-1997 (TREMELREL. 04, CREATED)
DT 01-JUL-1997 (TREMELREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE TNF RECEPTOR ASSOCIATED FACTOR 5 (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 97321041.
RA NAKANO H., SHINDO M., YAMADA K., YOSHIDA M.C., SANTEE S.M., WARE C.F.,
RA JENKINS N.A., GILBERT D.J., YAGITA H., COPELAND N.G., OKUMURA K.,
RL GENOMICS 42:26-32(1997).
CC -I- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL; U69108; G2138180; -.
DR PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
KW ZINC-FINGER.
FT NON_TER.
SQ SEQUENCE 538 AA; 62238 MW; 57B3F125 CRC32;

Query Match 50.7%; Score 894; DB 2; Length 538;
Best Local Similarity 59.2%; Pred. No. 7.96e-150;
Matches 113; Conservative 47; Mismatches 28; Indels 3; Gaps 2;

Db 348 AVLEETNKHDTHINIKHAOLSKNEERFKLEGTGCVNGKLWKVDYKMKREAYDGHV 407
QY 378 GLLESLSRHDTLSVHDRLADMDLRFQVLETASVNGVLWKIRDYKRRKQAVMGKTL 437
Db 408 SIFSQSYTSRCYRLCARAYLNGDGSGRGSHLSLYFVVMRGEFDSLLQWPFQRVRLML 467
QY 438 SLYSQPFYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRGEYDALLPWFQKQVTLML 497
Db 468 LDQ-SGKNIMETFKPDPPNSSFSFKPTGEMNIASGCPREVAHSVLENKAKYIKDDTLFL 526
QY 498 MDQSGRRRLHGDFAKPDPPNSSFSFKPTGEMNIASGCPVFAQTVLENG--TYIKDDTIFI 555
Db 527 KVAVDLTDLED 537
QY 556 KVIYDTSDLPD 566

RESULT 10
ID Q13077 PRELIMINARY; PRT; 416 AA.
AC Q13077.
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMELREL. 01, LAST ANNOTATION UPDATE)
DE EPSTEIN-BARR VIRUS-INDUCED PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOID TUMOR;
RA MOSIALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C.,
RA KIEFF E.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U19261; G673462; -.
SQ SEQUENCE 416 AA; 46163 MW; 760442BC CRC32;

Query Match 41.4%; Score 730; DB 2; Length 416;
Best Local Similarity 51.3%; Pred. No. 1.01e-116;
Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;

Db 222 SQDDRILSLRQVVELQOTLAQDQALGKLEQSLRLMEASFDGTFWKTNTVTRRCH 281
QY 371 GQAARNTGL-LESQLSRHDTLSVHDRLADMDLRFQVLETASVNGVLWKIRDYKRRKQ 429
Db 282 ESACGRVSLFSPAFYAKYKYLCLRLYLINGDGTGKTRHLSLFLVIMRGEYDALLPWF 341
QY 430 EAVMGKTLISQPFYTGFGYKMCARVYLNGDGMKGTHLSLFFVIMRGEYDALLPWF 489
Db 342 RNKVTFMLDQ-NNREHAIDAFRDLSSASFQRPQSETNVASGCPFLFFLSKLQSPKHAY 400
QY 490 KQKVTMLMDQSGSSRRHLGDFAKPDPPNSSFSFKPTGEMNIASGCPVFAQTVLENG--TY 547
Db 401 VKDITMLKCIIVETS 415
QY 548 IKDDTIFIKVIDTS 562

RESULT 11
ID Q12933 PRELIMINARY; PRT; 501 AA.
AC Q12933.
DT 01-NOV-1996 (TREMELREL. 01, CREATED)
DT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3.
GN TRAF3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9536558.
RA SONG H.Y., DONNER D.B.;
RL BIOCHEM. J. 309:825-829(1995).
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QY 402 DLRFQVLE-TASYNGVLWIKIRYDKRRKQEAVMGKTLISLQSPFYGYFGYKMCARVYLN 460

Db 354 GNGSGEGTHSLYIRVLPGAFDNLLEWPFARRVTFSLDQSDPLAKPQHVTTFHPDPN 413

QY 461 GDMGKGTHLSLFFVIMRGEVDALLPWFQKVTLMMDQG--S-SR-RHLGDAFAPDPN 516

Db 414 WNKFOKPGTWGSLDESGLFGYKPFKFIHQDIRKNRYVRDADFVIRAAVE 463

QY 517 SSSFKKP-T-GEMNIAS--GCPVFAQTVLENGTYIKDDTIFIKVIVD 560

RESULT 13

ID Q61382 PRELIMINARY; PRT; 470 AA.

AC Q61382;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE CYSTEINE RICH MOTIF ASSOCIATED TO RING AND TRAF DOMAINS PROTEIN

DE (MCARTI).

GN GN CART1.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

EN [1]

RP SEQUENCE FROM N.A.

RA REGNER C.H.;

RL SUBMITTED (OCT-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL: X92346; G1041446; -

DR PROSITE: PS00518; ZINC\_FINGER\_C3HC4; 1.

KW ZINC-FINGER.

SQ SEQUENCE 470 AA; 53418 MW; 42968389 CRC32;

Query Match 23.1%; Score 407; DB 10; Length 470;

Best Local Similarity 38.1%; Pred. No. 3,02e-53;

Matches 66; Conservative 45; Mismatches 48; Indels 11; Gaps

Db 294 ELRBELEELISGSDVLWIKGSGYRRLOEAKAPNLECFSPAFYTHYGYKLQVSASLN 353

QY 402 DLRFQVLE-TASYNGVLWIKIRYDKRRKQEAVMGKTLISLQSPFYGYFGYKMCARVYLN 460

Db 354 GNGSGEGTHSLYIRVLPGAFDNLLEWPFARRVTFSLDQSDPLAKPQHVTTFHPDPN 413

QY 461 GDMGKGTHLSLFFVIMRGEVDALLPWFQKVTLMMDQG--S-SR-RHLGDAFAPDPN 516

Db 414 WNKFOKPGTWGSLDESGLFGYKPFKFIHQDIRKNRYVRDADFVIRASVE 463

QY 517 SSSFKKP-T-GEMNIAS--GCPVFAQTVLENGTYIKDDTIFIKVIVD 560

RESULT 14

ID P70196 PRELIMINARY; PRT; 530 AA.

AC P70196;

DT 01-FEB-1997 (TREMBLREL. 02, CREATED)

DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE TNF RECEPTOR-ASSOCIATED FACTOR 6 (TRAF6).

DE GN TRAF6.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

EN [1]

RP SEQUENCE FROM N.A.

RA ISHIDA T., WATZUSHIMA S., AZUMA S., KOBAYASHI N., TOJO T., SUZUKI K.,

RA AIZAWA S., MIYANABE T., MOSTALOS G., KIEFF E., YAMAMOTO T., INOUE J.;

J. BIOL. CHEM. 271:28745-28748(1996)

CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL: D84655; G1651195; -

DR MGD; MGI-108072; TRAF6.

DR PROSITE; PS00518; ZINC\_FINGER\_C3HC4; 1.

KW ZINC-FINGER.

SQ SEQUENCE 530 AA; 60082 MW; C59CCCFER CRC32;

US-08-813-323A-1-03.rspt

Mon Aug 10 10:47:15 1998

Query Match 19.1%; Score 337; DB 10; Length 530;  
 Best Local Similarity 30.5%; Pred. No. 4.59e-40; Indels 9; Gaps 8;  
 Matches 64; Conservative 46; Mismatches 91; Indels 9; Gaps 8;  
 Db 304 EETIKQLESRLVRQDHQIRELTAKMETQ-SMYVGELK-RTIRTE-D-KVAEMEAOQCNG 359  
 QY 357 QNRVTELESVDKSAQAARN-TGLESQSLRDQTLSDHDIRLADMDLRQVLETASYNG 415  
 Db 360 IYIKWIGFQMHKSGEERPVVHSPGFTTGRGKLCMLHLQLPTAORCANYISLFV 419  
 QY 416 VLIWKIRDYKRRKQEAAMGKTLISYQPFYGYGKMCARVYLNQDGMKG-GTHLSLEF 474  
 Db 420 HYMQEYDHLWPFGQIRTLTILDSALIRQNHVEEYMDAKPELLAFORPTIPRNPKEG 479  
 QY 475 VIMRGEYDALLPFPFKQKVTLMMDQSS--RRHLGDAFKDPDNNSSFFKPKPTGEMNIAS- 531  
 Db 480 GYVTFMHLRALRQGTIFIKDDTLVRCVST 509  
 QY 532 GCPVFAQTGLENGTYIKDDTIFIKVIVDT 561

RESULT 15  
 ID 016188 PRELIMINARY; PRT: 284 AA.  
 AC 016188;  
 DT 01-JAN-1998 (TREMBREL. 05, CREATED)  
 DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)  
 DT 01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)  
 DE TROPOMYOSIN.  
 OS DERMATOPHAGOIDES PTERONYSSINUS (HOUSE-DUST MITE).  
 OC EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ACARI.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SMITH W. MILLS K.L., THOMAS W.R.:  
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
 DR EMBL; AF016278; G2353266;  
 DR PROSITE; PS00326; TROPOMYOSIN; 1.  
 SQ SEQUENCE 284 AA; 32973 MW; E1BAF90B CRC32;

Query Match 6.6%; Score 117; DB 3; Length 284;  
 Best Local Similarity 17.3%; Pred. No. 7.04e-03;  
 Matches 13; Conservative 26; Mismatches 35; Indels 1; Gaps 1;  
 Db 41 BEVRALOKKIQIENELDQVOEQLSAANTKLEEKALQTAEGDVAALNRRIOLEEDLE 100  
 QY 327 EKLKELDKIIRPFQNWEEA-DSMKSSVESLQNRVTELESVDKSAQAARNYGLLESQLS 385  
 Db 101 RSEERLKIATAKLEE 115  
 QY 386 RHDQTLSDHDIRLAD 400

Search completed: Thu Aug 6 14:09:57 1998  
 Job time : 89 secs.